Claim Amendments

Please amend the claims as follows:

Claims 1-13 (canceled)

- Claim 14 (currently amended) A method of identifying one or more nucleic acids comprising:
 - a) obtaining a probe for each nucleic acid to be identified;
 - b) labeling each probe with attaching at least one carbon nanotube to each probe;
 - c) hybridizing the probes to the nucleic acids;
 - d) exciting the nanotubes; and
 - e) detecting the emission spectra of the excited nanotubes.
- Claim 15 (original) The method of claim 14, wherein the nanotubes are excited with an ultraviolet (UV) laser or an electron beam.
- Claim 16 (original) The method of claim 15, further comprising identifying one or more peaks in the optical emission spectrum of each nanotube.
- Claim 17 (original) The method of claim 16, further comprising determining the wavelength of each peak.
- Claim 18 (previously presented) The method of claim 14, wherein at least one probe is attached to at least two nanotubes.

Claim 19 (canceled)

Claim 20 (canceled)

- Claim 31 (previously presented) The method of claim 14, wherein the nanotubes are single wall carbon nanotubes.
- Claim 32 (previously presented) The method of claim 14, wherein nanotubes attached to different probes exhibit distinguishable emission spectra.
- Claim 33 (previously presented) The method of claim 14, wherein the probes are oligonucleotides, chemically modified oligonucleotides, oligonucleotide analogs or peptide nucleic acids.
- Claim 34 (previously presented) The method of claim 33, wherein the probes comprise all possible nucleotide sequences for a probe of defined length.

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- Claim 35 (previously presented) The method of claim 34, wherein the probe length is selected from the group consisting of 4, 5, 6, 7 and 8 nucleotides.
- Claim 36 (currently amended) The method of claim 33, wherein at least one probe is attached to labeled with at least two nanotubes.
- Claim 37 (previously presented) The method of claim 33, wherein the probes comprise random nucleotide sequences.
- Claim 38 (previously presented) The method of claim 33, wherein the probes comprise at least one constant nucleotide.
- Claim 39 (previously presented) The method of claim 33, wherein the probe length is selected from the group consisting of 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14 and 15 nucleotides.
- Claim 40 (withdrawn) The method of claim 33, wherein the probe length is greater than 15 nucleotides.
- Claim 41 (canceled)
- Claim 42 (previously presented) The method of claim 14, further comprising identifying the probes that hybridize with the nucleic acid.
- Claim 43 (previously presented) The method of claim 14, wherein the nucleic acids are attached to a substrate.
- Claim 44 (previously presented) The method of claim 43, wherein the substrate is a chip.
- Claim 45 (previously presented) The method of claim 42, further comprising identifying the sequence of probes that are hybridized with the nucleic acid.
- Claim 46 (previously presented) The method of claim 45, further comprising moving the hybridized nucleic acid past a detector, wherein the hybridized probes move past the detector in a linear sequence.
- Claim 47 (previously presented) The method of claim 46, wherein the hybridized nucleic acid moves past the detector in a microchannel or microcapillary.
- Claim 48 (previously presented) The method of claim 45, further comprising separating unhybridized probes from probes hybridized to the nucleic acid.

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